Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

<223>

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=12; day=14; hr=7; min=32; sec=9; ms=100;]

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Xaa at positon 10 may be Lys, Arg or Thr

Trp Leu Xaa Glu Val Xaa Xaa Xaa Tyr Xaa Leu

Several errors above: the "<213> Unknown" requires an explanation in a "<220>-<223>" section under it; although the "<213>" response is "Unknown", please try to indicate the source of the genetic material ("Unknown" would not be a sufficient explanation). Please number the amino acids under every 5 amino acids, beginning with "1"; do not use TAB codes between amino acid numbers. TABs cause misaligned numbers. Same errors in Sequence 7.

<210> 8

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<220>

<400> 8

Trp Leu Val Glu Val Ser Glu Glu Tyr Lys Leu Val Ser Asp Thr

Please number the above amino acids; please remove the "<220>", since no <221>, <222>, or <223> is shown. Same errors in Sequences 9-31.

<210> 29

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<220>

<400> 29

Glu Leu Ser Met Leu Asp Tyr Gln Ser Val Lys Phe Leu Pro ser

Please: 1) remove the <220>; 2) number the amino acids; 3) replace "ser" at location 15 with "Ser"

Validated By CRFValidator v 1.0.3

Application No: 10584024 Version No: 2.0

Input Set:

Output Set:

Started: 2010-12-03 12:58:28.054 **Finished:** 2010-12-03 12:58:29.111

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 57 ms

Total Warnings: 6
Total Errors: 3

No. of SeqIDs Defined: 31

Actual SeqID Count: 31

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Ţ	W	213	Artificial or Unknown found in <213> in SEQ ID (5)								
Ī	W	213	Artificial or Unknown found in <213> in SEQ ID (6)								
]	E	224	<220>, $<223>$ section required as $<213>$ has Artificial sequence or Unknown in SEQID (6)								
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Ala Lys Lys Ala Met Gly Arg Gly Val Ser Ile Pro Pro Thr Lys Pro 35 40 45

Ser Phe Lys Gln Gln Lys Arg Arg Ala Val Leu Lys Asp Val Ser Asn 50 55 60

Thr Ser Ala Asp Ile Ile Tyr Ser Glu Leu Arg Lys Gly Gly Asn Ile 65 70 75 80

Lys Ala Asn Arg Lys Cys Leu Lys Glu Pro Lys Lys Ala Ala Lys Glu

90 95

Gly Ala Asn	Ser Ala 100	Met Asp	Ile	Leu 105	Val	Asp	Met	His	Thr 110	Glu	Lys
Ser Lys Leu 115	Ala Glu	Asp Leu	Ser 120	Lys	Ile	Arg	Met	Ala 125	Glu	Ala	Gln
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Ser Asn Val	Glu Asp 165	Pro Gln	Суз	Cys	Ser 170	Leu	Tyr	Ala	Ala	Asp 175	Ile
Tyr Asp Asn	Ile His 180	Val Ala	Glu	Leu 185	Gln	Gln	Arg	Pro	Leu 190	Ala	Asn
Tyr Met Glu 195	Leu Val	Gln Arg	Asp 200	Ile	Asp	Pro	Asp	Met 205	Arg	Lys	Ile
Leu Ile Asp 210	Trp Leu	Val Glu 215	Val	Ser	Asp	Asp	Tyr 220	Lys	Leu	Val	Pro
Asp Thr Leu 225	Tyr Leu	Thr Val	Asn	Leu	Ile	Asp 235	Arg	Phe	Leu	Ser	Asn 240
Ser Tyr Ile	Glu Arg 245	Gln Arg	Leu	Gln	Leu 250	Leu	Gly	Val	Ser	Cys 255	Met
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Phe Cys Phe 275	Ile Thr	Ala Asn	Thr 280	Tyr	Thr	Arg	Pro	Glu 285	Val	Leu	Ser
Met Glu Ile 290	Gln Ile	Leu Asn 295	Phe	Val	His	Phe	Arg 300	Leu	Ser	Val	Pro
Thr Thr Lys	Thr Phe	Leu Arg 310	Arg	Phe	Ile	Lys 315	Ala	Ala	Gln	Ala	Ser 320

Tyr Lys Val Pro Phe Ile Glu Leu Glu Tyr Leu Ala Asn Tyr Leu Ala 325 330 335

340 345 350

Ile Ala Ala Ser Ala Val Phe Leu Ala Arg Trp Thr Leu Asp Gln Thr 355 360 365

Asp His Pro Trp Asn Pro Thr Leu Gln His Tyr Thr Arg Tyr Glu Val 370 375 380

Ala Glu Leu Lys Asn Thr Val Leu Ala Met Glu Asp Leu Gln Leu Asn 385 390 395 400

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